AMENDMENTS TO THE CLAIMS

1. (Previously presented) A method for identifying analytes that induce a third expression profile that is more similar to a first expression profile than is a second expression profile, comprising:

(a) performing an assay to obtain a first expression profile of a set of representative molecules in a first biological sample;

(b) performing an assay to obtain a second expression profile of the set of molecules in a second biological sample, wherein the second biological sample differs from the first biological sample by a known parameter;

(c) performing an assay to obtain a third expression profile of the set of molecules in the second biological sample after treatment of the second biological sample with at least one analyte of previously uncharacterized specific pharmacological activity; and

(d) comparing the third expression profile with the first and second expression profiles to identify one or more analytes that induces a third expression profile that is more similar to the first expression profile than is the second expression profile, wherein the analytes identified as inducing a third expression profile that is more similar to the first expression profile than is a second expression profile is indicative of the identified analytes possessing pharmacological activity.

2. (Currently amended) The method of Claim 1, wherein step (d) comprises:

(a) deriving a first difference profile by comparing the first expression profile with the second expression profile;

(b) deriving a second difference profile by comparing the second expression profile with the third expression profile; and

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(c) comparing the first difference profile with the second difference profile to identify the one or more analytes possessing pharmacological activity.

3. (Currently amended) The method of Claim 1, wherein identification of the one or more analytes with pharmacological activity comprises classifying ~~all~~ the expression profiles obtained in steps (a), (b) and (c) using neural network computing.

4. (Currently amended) The method of Claim 1, wherein any of the ~~steps used to perform the assay comprises use of~~ assays are performed using serial analysis of gene expression.

5. (Canceled)

6. (Original) The method of Claim 1, wherein the first or second biological sample is selected from one or more of the group of a specific cell type in vitro, a combination of cell types in vitro, a specific tissue type in vitro, a combination of tissue types in vitro, organs in vitro, a specific cell type in vivo, a combination of cell types in vivo, a specific tissue type in vivo, a combination of tissue types in vivo, organs in vivo, and an entire single-celled or multicellular organism.

7. (Previously presented) The method of Claim 1, wherein at least one biological sample is derived from a sample that exhibits a disease condition.

8. (Previously presented) The method of Claim 1, wherein the representative molecules are selected from the group consisting of mRNA transcripts or cDNA derived therefrom, proteins, phosphoproteins, carbohydrates, and lipids.

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9. (Currently amended) The method of Claim 1, wherein any of the ~~steps used to perform at least one of the assays comprises use of~~ assays are performed using polynucleic acid microarrays.

10. (Previously presented) The method of Claim 9, wherein the polynucleic acid microarrays comprise elements capable of differentially binding specific peptides.

11. (Currently amended) The method of Claim 1, wherein ~~any steps used to perform~~ performance of at least one of the assays comprises simultaneously detecting the rates of transcriptions of multiple genes.

12. (Currently amended) The method of Claim 1, wherein any ~~steps used to perform at least one~~ of the assays ~~comprises use of~~ are performed using capillary electrophoresis.

13. (Currently amended) The method of Claim 1, wherein any ~~steps used to perform at least one~~ of the assays ~~comprises use of~~ are performed using 2-dimensional gel electrophoreses.

14. (Currently amended) The method of Claim 1, wherein any ~~steps used to perform at least~~ one of the assays ~~comprises use of~~ are performed using one or more antibodies.

15. (Currently amended) The method of Claim 1, wherein any ~~steps used to perform at least one~~ of the assays ~~comprises use of~~ are performed using spectrometry techniques.

16. (Original) The method of Claim 15, wherein the spectrometry technique is mass spectrometry.

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17. (Currently amended) The method of Claim 1, wherein any ~~steps used to perform at least one~~ of the assays ~~comprises use of~~ are performed using a method selected from the group consisting of fiber-optic, bead-based mRNA and protein detection.

18. (Currently amended) The method of Claim 1, wherein any ~~steps used to perform at least one~~ of the assays ~~comprises use of~~ are performed using differential display.

19. (Previously presented) The method of Claim 1, wherein step (c) is conducted many times in high-throughput fashion with distinct analytes from a library of analytes.

20. (Previously presented) The method of Claim 1, wherein the first expression profile of step (a) is derived from a combination of biological samples.

21. (Original) The method of Claim 1, wherein the tested analyte of step (c) possesses previously characterized pharmacological activity unrelated to the parameter by which the first and second biological samples are known to differ, and where its pharmacological activity relative to said parameter is previously uncharacterized.

22. (Withdrawn - currently amended) The method of Claim 1, wherein any ~~steps used to perform at least one~~ of the assays ~~comprises use of~~ are performed using chromatographic techniques.

23. (Original) The method of Claim 22, wherein the chromatographic technique is HPLC.

24. (Original) The method of Claim 22, wherein the chromatographic technique is gas chromatography.

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25. (Withdrawn - currently amended) The method of Claim 1, wherein any ~~steps used to perform at least one~~ of the assays ~~comprises use of~~ are performed using Western blotting.

26-31. (Canceled)

32. (Previously presented) A method for identifying analytes that induce a third expression profile that is more similar to a first expression profile than is a second expression profile, comprising:

(a) performing an assay to obtain a first expression profile of a set of representative molecules in a first biological sample;

(b) performing an assay to obtain a second expression profile of the set of molecules in a second biological sample, wherein the second biological sample differs from the first biological sample by exposure to a drug treatment;

(c) performing an assay to obtain a third expression profile of the set of molecules in a third biological sample after treatment of the third biological sample with at least one analyte of previously uncharacterized specific pharmacological activity with respect to the drug treatment to which the second biological sample was exposed; and

(d) comparing the third expression profile with the first and second expression profiles to identify one or more analytes that induces a third expression profile that is more similar to the first expression profile than is the second expression profile, wherein the analytes identified as inducing a third expression profile that is more similar to the first expression profile than is the second expression profile is indicative of the identified analytes possessing pharmacological activity with respect to the drug treatment.

33. (Currently amended) The method of Claim 32, wherein identification of the one or more analytes with pharmacological activity with respect to the drug treatment comprises

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classifying [[all]] the expression profiles obtained in steps (a), (b) and (c) using neural network computing.

34. (Currently amended) The method of Claim 32, wherein any of the ~~steps used to perform at least one of the~~ assays ~~comprises use of~~ are performed using serial analysis of gene expression.

35. (Previously presented) The method of Claim 32, wherein the biological sample is selected from one or more of the group of a specific cell type in vitro, a combination of cell types in vitro, a specific tissue type in vitro, a combination of tissue types in vitro, organs in vitro, a specific cell type in vivo, a combination of cell types in vivo, a specific tissue type in vivo, a combination of tissue types in vivo, organs in vivo, and an entire single-celled or multicellular organism.

36. (Currently amended) The method of Claim 32, wherein any of the ~~steps used to perform at least one of the~~ assays ~~comprises use of~~ are performed using polynucleic acid microarrays.

37. (Previously presented) The method of Claim 32, wherein step (b) is conducted many times in high-throughput fashion with distinct analytes from a library of analytes.

38. (Previously presented) The method of Claim 1, wherein the representative molecules are mRNA transcripts.

39. (Previously presented) The method of Claim 1, wherein the representative molecules are cDNA derived from mRNA transcripts.

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40. (Previously presented) The method of Claim 1, wherein the representative molecules are proteins.

41. (Previously presented) The method of Claim 1, wherein the representative molecules are phosphoproteins.

42. (Previously presented) The method of Claim 1, wherein the representative molecules are carbohydrates.

43. (Previously presented) The method of Claim 1, wherein the representative molecules are lipids.

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